Claims

1. A transgenic *Brassica* plant, or seed, cells or tissues thereof, characterized by one or both of the following characteristics:

a) the genomic DNA is capable of yielding at least two of the restriction fragments or sets of restriction fragments selected from the group consisting of:

i) one set of NcoI fragments, one with a length of between 5077 and 14057 bp, and one with a length of between 2450 and 2838 bp;

ii) one set of EcoRV fragments wherein one has a length of between 5077 and 14057 bp, and one with a length of between 4507 and 5077 bp;

iii) one set of MunI fragments, one with a length of between 5077 and 14057 bp, and one with a length of between 2838 and 4799 bp;

iv) one HindIII fragment, with a length of between 2838 and 4507 bp;

v) one EcoRI fragment, with a length of between 1989 and 2450 bp;

wherein each of the restriction fragments is capable of hybridizing under standard stringency conditions, with the +/- 2000 bp fragment obtainable by PCR amplification of a fragment of SEQ ID NO:1, using the probes having the nucleotide sequence of SEQ ID NO:2 and SEQ ID NO:3 respectively and/or

b) the genomic DNA can be used to amplify a DNA fragment of between 160 and 200 bp, using a polymerase chain reaction with two primers having the nucleotide sequence of SEQ ID NO:11 and SEQ ID NO:12 respectively.

2. The transgenic *Brassica* plant, or seed, cells or tissues thereof according to claim 1, the genomic DNA of which is capable of yielding at least two of the restriction fragments or sets of restriction fragments selected from the group consisting of:

i) one set of NcoI fragments, one with a length of between 5077 and 14057 bp, and one with a length of between 2450 and 2838 bp;

ii) one set of EcoRV fragments, one with a length of between 5077 and 14057 bp, and one with a length of between 4507 and 5077 bp;

iii) one set of MunI fragments, one with a length of between 5077 and 14057 bp, and one with a length of between 2838 and 4799 bp;

iv) one HindIII fragment, with a length of between 2838 and 4507 bp;

v) one EcoRI fragment, with a length of between 1989 and 2450 bp;

wherein each of the restriction fragments is capable of hybridizing under standard stringency conditions, with the +/- 2000 bp fragment obtainable by PCR amplification of a fragment of SEQ ID NO:1, using the probes having the nucleotide sequence of SEQ ID NO:2 and SEQ ID NO:3 respectively.

3. The *Brassica* plant, or seed, cells or tissues thereof according to claim 2, the genomic DNA of which is capable of yielding at least three of said restriction fragments or sets of restriction fragments.

4. The *Brassica* plant, or seed, cells or tissues thereof according to claim 3, the genomic DNA of which is capable of yielding at least four of said restriction fragments or sets of restriction fragments.

5. The *Brassica* plant, or seed, cells or tissues thereof according to claim 4, the genomic DNA of which is capable of yielding all five of said restriction fragments or sets of restriction fragments.

6. The *Brassica* plant, or seed, cells or tissues thereof, according to claim 1, the genomic DNA of which can be used to amplify a DNA fragment of between 160 and

200 bp, using a polymerase chain reaction with two primers having the nucleotide sequence of SEQ ID NO:11 and SEQ ID NO:12 respectively.

7. The *Brassica* plant, or seed, cells or tissues thereof, according to claim 6, the genomic DNA of which can be used to amplify a DNA fragment of about 183 bp, using a polymerase chain reaction with two primers having the nucleotide sequence of SEQ ID NO:11 and SEQ ID NO:12 respectively.

8. The *Brassica* plant, or seed, cells or tissues thereof, according to claim 1, which can be grown from the seed deposited at the ATCC under accession number PTA-850 or PTA-2485.

9. The *Brassica* plant, or seed, cells or tissues thereof, which can be obtained by propagation of and/or breeding with a *Brassica* plant grown from the seed deposited at the ATCC under ATCC accession number PTA-850 or PTA-2485.

10. The *Brassica* plant claim 1, wherein said plant is male-sterile.

11. Transgenic plants, seeds, cells or tissues, the genomic DNA of which comprises a transgene integrated into the chromosomal DNA in a region which comprises a sequence of at least 40 bp having at least 85% sequence identity with the plant DNA sequences within SEQ ID NO:8 and/or SEQ ID NO:10.

12. A process for producing a transgenic *Brassica* plant or cell or tissue of a *Brassica* plant, said process comprising introducing a recombinant DNA molecule into a region of its chromosomal DNA corresponding to a sequence of at least 40 bp having at least 85% sequence identity with the plant DNA sequences within SEQ ID NO:8 and/or SEQ ID NO:10, and, optionally, regenerating a *Brassica* plant from the transformed *Brassica* cell or tissue.

13. The process of claim 12, wherein said transgene comprises a male-sterility gene.

14. A method for identifying a transgenic plant, or cells or tissues thereof, comprising the elite event MS-B2, which method comprises establishing one or both of the following characteristics:

a) the genomic DNA is capable of yielding at least two of the restriction fragments or sets of restriction fragments selected from the group consisting of:

i) one set of NcoI fragments, one with a length of between 5077 and 14057 bp, and one with a length of between 2450 and 2838 bp;

ii) one set of EcoRV fragments wherein one has a length of between 5077 and 14057 bp and one with a length of between 4507 and 5077 bp;

iii) one set of MunI fragments, one with a length of between 5077 and 14057 bp and one with a length of between 2838 and 4799 bp;

iv) one HindIII fragment, with a length of between 2838 and 4507 bp;

v) one EcoRI fragment, with a length of between 1989 and 2450 bp;

wherein each of the restriction fragments is capable of hybridizing under standard stringency conditions, with the +/- 2000 bp fragment obtainable by PCR amplification of

a fragment of SEQ ID NO:1, using the probes having the nucleotide sequence of SEQ ID NO:2 and SEQ ID NO:3 respectively and/or

b) the genomic DNA can be used to amplify a DNA fragment of between 160 and 200 bp, using a polymerase chain reaction with two primers having the nucleotide sequence of SEQ ID NO:11 and SEQ ID NO:12 respectively.

15. The method of claim 14, which comprises establishing whether the genomic DNA is capable of yielding all five of said restriction fragments or sets of restriction fragments.

16. The method of claim 14, which comprises establishing whether the genomic DNA of the transgenic plant, or its cells or tissues can be used to amplify a DNA fragment of about 183 bp, using a polymerase chain reaction with two primers having the nucleotide sequence of SEQ ID NO:11 and SEQ ID NO:12, respectively.

17. A kit for identifying a transgenic plant, its cells or tissues comprising the MS-B2 elite event, said kit comprising at least two PCR probes, one of which recognizes a sequence within the foreign DNA of MS-B2, the other which recognizes a sequence within the 3' or 5' border flanking region of MS-B2.

18. A kit for identifying a transgenic plant, its cells or tissues comprising the MS-B2 elite event, said kit comprising the PCR probes having the nucleotide sequence of SEQ ID NO:11 and SEQ ID NO:12 for use in a PCR identification protocol.

19. The seed deposited at the ATCC under accession number PTA-850 or PTA-2485.

20. A process for producing hybrid seed, which process comprises crossing the male-sterile *Brassica* plant of claim 10, with a male-fertile *Brassica* plant, and harvesting hybrid seed from said male-sterile plant.

21. A plant, cell, tissue or progeny grown from the seed as claimed in claim 19.

22. A plant obtained by propagation of and/or breeding with a *Brassica* plant grown from the seed as claimed in claim 19.

add B1

add D3